



1	GTGACGCGATGGAGTGGTAGCCGAGGAGGAAGC	ATG	CTG	GCC	GTC	GGC	TGC	GGG	CTG	CTG	GCT	63									
1		M	L	A	V	G	C	A	L	L	A	10									
64	GCC	CTG	CTG	GCC	GCG	CCG	GGA	GCG	GCG	CTG	GCC	CCA	AGG	CGC	TGC	CCT	GCG	CAG	GAG	GTG	123
11	A	L	L	A	A	P	G	A	A	L	A	P	R	R	C	P	A	Q	E	V	30
124	GCA	AGA	GGC	GTG	CTG	ACC	AGT	CTG	CCA	GGA	GAC	AGC	GTG	ACT	CTG	ACC	TGC	CCG	GGG	GTA	183
31	A	R	G	V	L	T	S	L	P	G	D	S	V	T	L	T	C	P	G	V	50
184	GAG	CCG	GAA	GAC	AAT	GCC	ACT	GTT	CAC	TGG	GTG	CTC	AGG	AAG	CCG	GCT	GCA	GGC	TCC	CAC	243
51	E	P	E	D	N	A	T	V	H	W	V	L	R	K	P	A	A	G	S	H	70
244	CCC	AGC	AGA	TGG	GCT	GGC	ATG	GGA	AGG	AGG	CTG	CTG	CTG	AGG	TCG	GTG	CAG	CTC	CAC	GAC	303
71	P	S	R	W	A	G	M	G	R	R	L	L	L	R	S	V	Q	L	H	D	90
304	TCT	GGA	AAC	TAT	TCA	TGC	TAC	CGG	GCC	GGC	CGC	CCA	GCT	GGG	ACT	GTG	CAC	TTG	CTG	GTG	363
91	S	G	N	Y	S	C	Y	R	A	G	R	P	A	G	T	V	H	L	L	V	110
364	GAT	GTT	CCC	CCC	GAG	GAG	CCC	CAG	CTC	TCC	TGC	TTC	CGG	AAG	AGC	CCC	CTC	AGC	AAT	GTT	423
111	D	V	P	P	E	E	P	Q	L	S	C	F	R	K	S	P	L	S	N	V	130
424	GTT	TGT	GAG	TGG	GGT	CCT	CGG	AGC	ACC	CCA	TCC	CTG	ACG	ACA	AAG	GCT	GTG	CTC	TTG	GTG	483
131	V	C	E	W	G	P	R	S	T	P	S	L	T	T	K	A	V	L	L	V	150
484	AGG	AAG	TTT	CAG	AAC	AGT	CCG	GCC	GAA	GAC	TTC	CAG	GAG	CCG	TGC	CAG	TAT	TCC	CAG	GAG	543
151	R	K	F	Q	N	S	P	A	E	D	F	Q	E	P	C	Q	Y	S	Q	E	170
544	TCC	CAG	AAG	TTC	TCC	TGC	CAG	TTA	GCA	GTC	CCG	GAG	GGA	GAC	AGC	TCT	TTC	TAC	ATA	GTG	603
171	S	Q	K	F	S	C	Q	L	A	V	P	E	G	D	S	S	F	Y	I	V	190
604	TCC	ATG	TGC	GTC	GCC	AGT	AGT	GTC	GGG	AGC	AAG	TTC	AGC	AAA	ACT	CAA	ACC	TTT	CAG	GGT	663
191	S	M	C	V	A	S	S	V	G	S	K	F	S	K	T	Q	T	F	Q	G	210
664	TGT	GGA	ATC	TTG	CAG	CCT	GAT	CCG	CCT	GCC	AAC	ATC	ACA	GTC	ACT	GCC	GTG	GCC	AGA	AAC	723
211	C	G	I	L	Q	P	D	P	P	A	N	I	T	V	T	A	V	A	R	N	230
724	CCC	CGC	TGG	CTC	AGT	GTC	ACC	TGG	CAA	GAC	CCC	CAC	TCC	TGG	AAC	TCA	TCT	TTC	TAC	AGA	783
231	P	R	W	L	S	V	T	W	Q	D	P	H	S	W	N	S	S	F	Y	R	250
784	CTA	CGG	TTT	GAG	CTC	AGA	TAT	CGG	GCT	GAA	CGG	TCA	AAG	ACA	TTC	ACA	ACA	TGG	ATG	GTC	843
251	L	R	F	E	L	R	Y	R	A	E	R	S	K	T	F	T	T	W	M	V	270
844	AAG	GAC	CTC	CAG	CAT	CAC	TGT	GTC	ATC	CAC	GAC	GCC	TGG	AGC	GGC	CTG	AGG	CAC	GTG	GTG	903
271	K	D	L	Q	H	H	C	V	I	H	D	A	W	S	G	L	R	H	V	V	290
904	CAG	CTT	CGT	GCC	CAG	GAG	GAG	TTC	GGG	CAA	GGC	GAG	TGG	AGC	GAG	TGG	AGC	CCG	GAG	GCC	963
291	Q	L	R	A	Q	E	E	F	G	Q	G	E	W	S	E	W	S	P	G	A	310
964	ATG	GGC	ACG	CCT	TGG	ACA	GAA	TCC	AGG	AGT	CCT	CCA	GCT	CGA	GGA	GGT	GGA	GGT	TCT	GGA	1023
311	M	G	T	P	W	T	E	S	R	S	P	P	A	R	G	G	G	G	S	G	330
1024	GGT	GGA	GGT	TCT	GGA	GGT	GGA	GGT	TCT	GTC	GAG	CCA	GTA	CCC	CCA	GGA	GAA	GAT	TCC	AAA	1083
331	G	G	G	S	G	G	G	G	S	V	E	P	V	P	P	G	E	D	S	K	350
1084	GAT	GTA	GCC	GCC	CCA	CAC	AGA	CAG	CCA	CTC	ACC	TCT	TCA	GAA	CGA	ATT	GAC	AAA	CAA	ATT	1143
351	D	V	A	A	P	H	R	Q	P	L	T	S	S	E	R	I	D	K	Q	I	370
1144	CGG	TAC	ATC	CTC	GAC	GGC	ATC	TCA	GCC	CTG	AGA	AAG	GAG	ACA	TGT	AAC	AAG	AGT	AAC	ATG	1203
371	R	Y	I	L	D	G	I	S	A	L	R	K	E	T	C	N	K	S	N	M	390
1204	TGT	GAA	AGC	AGC	AAA	GAG	GCA	CTG	GCA	GAA	AAC	AAC	CTG	AAC	CTT	CCA	AAG	ATG	GCT	GAA	1263
391	C	E	S	S	K	E	A	L	A	E	N	N	L	N	L	P	K	M	A	E	410
1264	AAA	GAT	GGA	TGC	TTC	CAA	TCT	GGA	TTC	AAT	GAG	GAG	ACT	TGC	CTG	GTG	AAA	ATC	ATC	ACT	1323
411	K	D	G	C	F	Q	S	G	F	N	E	E	T	C	L	V	K	I	I	T	430
1324	GGT	CTT	TTG	GAG	TTT	GAG	GTA	TAC	CTA	GAG	TAC	CTC	CAG	AAC	AGA	TTT	GAG	AGT	AGT	GAG	1383
431	G	L	L	E	F	E	V	Y	L	E	Y	L	Q	N	R	F	E	S	S	E	450
1384	GAA	CAA	GCC	AGA	GCT	GTG	CAG	ATG	AGT	ACA	AAA	GTC	CTG	ATC	CAG	TTC	CTG	CAG	AAA	AAG	1443
451	E	Q	A	R	A	V	Q	M	S	T	K	V	L	I	Q	F	L	Q	K	K	470
1444	GCA	AAG	AAT	CTA	GAT	GCA	ATA	ACC	ACC	CCT	GAC	CCA	ACC	ACA	AAT	GCC	AGC	CTG	CTG	ACG	1503
471	A	K	N	L	D	A	I	T	T	P	D	P	T	T	N	A	S	L	L	T	490
1504	AAG	CTG	CAG	GCA	CAG	AAC	CAG	TGG	CTG	CAG	GAC	ATG	ACA	ACT	CAT	CTC	ATT	CTG	CGC	AGC	1563
491	K	L	Q	A	Q	N	Q	W	L	Q	D	M	T	T	H	L	I	L	R	S	510
1564	TTT	AAG	GAG	TTC	CTG	CAG	TCC	AGC	CTG	AGG	GCT	CTT	CGG	CAA	ATG	TAG	CATGGGCACCGTCGAC				1627
511	F	K	E	F	L	Q	S	S	L	R	A	L	R	Q	M	*					525

[SEQ ID NO:1 and SEQ ID NO:2]

FIG. 1

REPLACEMENT SHEET

Appln. Filing Date: November 4, 1998

Title: CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS

Inventor(s): Rose-John Stefan

Appln. No.: 09/142,471

Sheet 2 of 4

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1  GTGACGC ATG GAG TGG TAG CCGAGGAGGAAGC ATG CTG GCC GTC GGC TGC GCG CTG CTG GCT 63
1  M L A V G C A L L A 10

64  GCC CTG CTG GCC GCG CCG GGA GCG GCG CTG GCC CCA AGG CGC TGC CCT GCG CAG GAG GTG 123
11  A L L A A P G A A L A P R R C P A Q E V 30

124  GCA AGA GGC GTG CTG ACC AGT CTG CCA GGA GAC AGC GTG ACT CTG ACC TGC CCG GGG GTA 183
31  A R G V L T S L P G D S V T L T C P G V 50

184  GAG CCG GAA GAC AAT GCC ACT GTT CAC TGG GTG CTC AGG AAG CCG GCT GCA GGC TCC CAC 243
51  E P E D N A T V H W V L R K P A A G S H 70

244  CCC AGC AGA TGG GCT GGC ATG GGA AGG AGG CTG CTG CTG AGG TCG GTG CAG CTC CAC GAC 303
71  P S R W A G M G R R L L L R S V Q L H D 90

304  TCT GGA AAC TAT TCA TGC TAC CGG GCC GGC GCG CCA GCT GGG ACT GTG CAC TTG CTG GTG 363
91  S G N Y S C Y R A G R P A G T V H L L V 110

364  GAT GTT CCC CCC GAG GAG CCC CAG CTC TCC TGC TTC CGG AAG AGC CCC CTC AGC AAT GTT 423
111  D V P P E G P Q L S C F R K S P L S N V 130

424  GTT TGT GAG TGG GGT CCT CGG AGC ACC CCA TCC CTG ACG ACA AAG GCT GTG CTC TTG GTG 483
131  V C E W G P R S T P S L T T K A V L L V 150

484  AGG AAG TTT CAG AAC AGT CCG GCC GAA GAC TTC CAG GAG CCG TGC CAG TAT TCC CAG GAG 543
151  R K F Q N S P A E D F Q E P C Q Y S Q E 170

544  TCC CAG AAG TTC TCC TGC CAG TTA GCA GTC CCG GAG GGA GAC AGC TCT TTC TAC ATA GTG 603
171  S Q K F S T G L A V P E G D S F Y I V 190

604  TCC ATG TGC GTC GCC AGT AGT GTC GGG AGC AAG TTC AGC AAA ACT CAA ACC TTT CAG GGT 663
191  S M C V A S S V G S K F S K T Q T F Q G 210

664  TGT GGA ATC TTG CAG CCT GAT CCG CCT GCC AAC ATC ACA GTC ACT GCC GTG GCC AGA AAC 723
211  C G I L Q P D P P A N I T V T A V A R N 230

724  CCC CGC TGG CTC AGT GTC ACC TGG CAA GAC CCC CAC TCC TGG AAC TCA TCT TTC TAC AGA 783
231  P R W L S V T W Q H S W N S S F Y R 250

784  CTA CGG TTT GAG CTC AGA TAT CGG GCT GAA CGG TCA AAG ACA TTC ACA ACA TGG ATG GTC 843
251  L R F E L R Y R A E R S K T F T T W M V 270

844  AAG GAC CTC CAG CAT CAC TGT GTC ATC CAC GAC GCC TGG AGC GGC CTG AGG CAC GTG GTG 903
271  K D L Q H H C V I H D A W S G L R H V V 290

904  CAG CTT CGT GCC CAG GAG GAG TTC GGG CAA GGC GAG TGG AGC GAG TGG AGC CCG GAG GCC 963
291  Q L R A Q E E F G Q G E W S E W S P E A 310

964  ATG GGC ACG CCT TGG ACA GAA TCC AGG AGT CCT CCA GCT CGA GGA GGT GGA GGT TCT GGA 1023
311  M G T P W T E S R S P P A R G G G G S G 330

1024  GGT GGA GGT TCT GTC GAG CCA GTA CCC CCA GGA GAA GAT TCC AAA GAT GTA GCC GCC CCA 1083
331  G G G S V E P V P P G E D S K D V A A P 350

1084  CAC AGA CAG CCA CTC ACC TCT TCA GAA CGA ATT GAC AAA CAA ATT CGG TAC ATC CTC GAC 1143
351  H R Q P L T S S E R I D K Q I R Y I L D 370

1144  GGC ATC TCA GCC CTG AGA AAG GAG ACA TGT AAC AAG AGT AAC ATG TGT GAA AGC AGC AAA 1203
371  G I S A L R K E T C N K S N M C E S S K 390

1204  GAG GCA CTG GCA GAA AAC AAC CTG AAC CTT CCA AAG ATG GCT GAA AAA GAT GGA TGC TTC 1263
391  E A L A E N N L N L P K M A E K D G C F 410

1264  CAA TCT GGA TTC AAT GAG GAG ACT TGC CTG GTG AAA ATC ATC ACT GGT CTT TTG GAG TTT 1323
411  Q S G F N E E T C L V K I I T G L L E F 430

1324  GAG GTA TAC CTA GAG TAC CTC CAG AAC AGA TTT GAG AGT AGT GAG GAA CAA GCC AGA GCT 1383
431  E V Y L E Y L Q N R F E S S E E Q A R A 450

1384  GTG CAG ATG AGT ACA AAA GTC CTG ATC CAG TTC CTG CAG AAA AAG GCA AAG AAT CTA GAT 1443
451  V Q M S T K V L I Q F L Q K K A K N L D 470

1444  GCA ATA ACC ACC CCT GAC CCA ACC ACA AAT GCC AGC CTG CTG ACG AAG CTG CAG GCA CAG 1503
471  A I T T P D P T T N A S L L T K L Q A Q 490

1504  AAC CAG TGG CTG CAG GAC ATG ACA ACT CAT CTC ATT CTG CGC AGC TTT AAG GAG TTC CTG 1563
491  N Q W L Q D M T T H L I L R S F K E F L 510

1564  CAG TCC AGC CTG AGG GCT CTT CGG CAA ATG TAG C ATG GGC ACC GTC GAC 1612
511  Q S S L R A L R Q M * 520

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[SEQ ID NO:3 and SEQ ID NO:4]

FIG. 2

REPLACEMENT SHEET

Appl. Filing Date: November 4, 1998

Title: CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN
PROTEINS

Inventor(s): Rose-John Stefan

Appl. No.: 09/142,471

Sheet 3 of 4

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Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu
Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro
1
Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr
5 10 15 20
Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile
25 30 35
Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
40 45 50
Ser Pro Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala
55 60 65
Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu
70 75 80
Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr
85 90 95 100
Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln
105 110 115
Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
120 125 130
Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu
135 140 145
Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Glu Asp Met Pro Thr His
150 155 160
Leu Ile Leu Arg Ser Leu Lys Glu Phe Leu Gln Arg Ser Leu Arg Ala
165 170 175 180
Leu Arg Gln Met
184

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[SEQ ID NO:5]

FIG. 3